



SEQUENCE LISTING

<110> Anderson, David
Peelle, Beau

<120> METHODS AND COMPOSITIONS COMPRISING RENILLA GFP

<130> A-68531-1/RMS/CYO

<140> US 09/710,058

<141> 2000-11-10

<150> US 60/164,592

<151> 1999-11-10

<160> 85

<170> PatentIn version 3.1

<210> 1

<211> 1079

<212> DNA

<213> Renilla muelleri

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<221> CDS

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acataatatc taagagacgc ctcattttaag agtagtaaaa atataatata tgatagagta 180

tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttggttaa tgcaatcgaa 240

agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta 291

Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
1 5 10

caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac 339

Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
15 20 25

cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc 387

His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
30 35 40

aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt 435

Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
45 50 55

gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc 483

Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe

60 65 70 75

acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca 531
 Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
 80 85 90

gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt 579
 Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
 95 100 105

gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac 627
 Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
 110 115 120

aga gtc gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg 675
 Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met
 125 130 135

cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg 723
 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
 140 145 150 155

aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac 771
 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
 160 165 170

tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa 819
 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
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ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg 867
 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
 190 195 200

gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act 915
 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
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gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac 963
 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
 220 225 230 235

gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca 1015
 Glu Trp Val

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aaaa 1079

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Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
35 40 45

Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60

Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
65 70 75 80

Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
85 90 95

Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
100 105 110

Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
115 120 125

Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
130 135 140

Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
145 150 155 160

Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
165 170 175

Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
180 185 190

Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
195 200 205

Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
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Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 225 230 235

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 <213> Ptilosarcus Gurneyi

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 cgggttacaa agggaggtcc gttgccattc gctttcgata ttgtttccat agctttccaa 240
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 ttcccggctg gatTTTTTcta cgaaagaaat ctacgctttg aagatggcgc cattgttgac 360
 attcgttcag atataagttt agaagatgat aagttccact acaaagtgga gtatagaggc 420
 aacggtttcc ctagtaacgg acccgtgatg caaaaagcca tcctcggcat ggagccatcg 480
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 gtgaaagaat tcccgaata tcactttatc catcatcgtc tggagaaaac ctacgtggaa 660
 gaaggaagct tcgtggaaca acacgagacg gccattgcac aactgaccac aattggaaaa 720
 cctctgggct cccttcatga atgggtgtag aaaatgacca atatactggg gaaaccgata 780
 accgtttgga agcttgtgta tacaaattat ttgggggtcat tttgtaatgt gtatgtgtgt 840
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 attaacgcgt ttcaaccagc agttggaatc tttaaaccga tcaaaactat taatataaat 1020
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Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe
15 20 25 30

tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg 144
Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu
35 40 45

atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac 192
Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp
50 55 60

att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac 240
Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr
65 70 75

cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt 288
Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe
80 85 90

ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att 336
Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile
95 100 105 110

cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag 384
Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu
115 120 125

tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc 432
Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala
130 135 140

atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc 480
Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly
145 150 155

gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac 528
Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn
160 165 170

tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg 576
Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val
175 180 185 190

aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc 624
Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr
195 200 205

tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca 672

Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala
 210 215 220

caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg 720
 Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 225 230 235

tagaaaatga ccaatatact ggggaaaatc accaatatac tggggaaaat gaccaattta 780

ctggggaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat 840

ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca 900

aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt 960

gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga 1020

cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc 1080

gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt 1140

aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata 1200

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Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
 35 40 45

Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
 50 55 60

Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
 65 70 75 80

Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
 85 90 95

Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110

Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125

Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
130 135 140

Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145 150 155 160

Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
165 170 175

Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
180 185 190

Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
195 200 205

Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
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Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225 230 235

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
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Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<223> "Xaa" at position 7 can be either Leu or Lys.

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<223> "Xaa" at position 8 can be either Asn or Phe.

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<223> "Xaa" at position 11 can be either Val or Leu.

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<223> "Xaa" at position 15 can be either Met or Leu.

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<223> "Xaa" at position 17 can be either Ala or Tyr.

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<223> "Xaa" at position 24 can be either Ile or Asp.

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<223> "Xaa" at position 37 can be either Lys or Glu.

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<223> "Xaa" at position 45 can be either Gln or Leu.

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<223> "Xaa" at position 56 can be either Pro or Lys.

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<223> "Xaa" at position 59 can be either Phe or Val.

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<223> "Xaa" at position 61 can be either Phe or Trp.

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<223> "Xaa" at position 73 can be either Arg or Gln.

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<223> "Xaa" at position 77 can be either Lys or Arg.

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<223> "Xaa" at position 87 can be either Tyr or Phe.

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<223> "Xaa" at position 90 can be either Gln or Ser.

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<223> "Xaa" at position 91 can be either Ala or Ser.

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<223> "Xaa" at position 92 can be either Phe or Met.

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<223> "Xaa" at position 98 can be either Gln or Tyr.

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<223> "Xaa" at position 105 can be either Glu or Lys.

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<223> "Xaa" at position 107 can be either Gly or Asp.

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<222> (110)..(110)
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<222> (112)..(112)
<223> "Xaa" at position 112 can be either Thr or Ile.

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<222> (114)..(114)

<223> "Xaa" at position 114 can be either Ser or Ala.

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<222> (115)..(115)

<223> "Xaa" at position 115 can be either Glu or Asp.

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<223> "Xaa" at position 116 can be either Ile or Val.

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<223> "Xaa" at position 118 can be either Leu or Phe.

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<222> (122)..(122)

<223> "Xaa" at position 122 can be either Lys or Thr.

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<223> "Xaa" at position 125 can be either Tyr or Asn.

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<223> "Xaa" at position 129 can be either Tyr or Leu.

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<223> "Xaa" at position 139 can be either Pro or Asn.

<220>
<221> MISC_FEATURE
<222> (140)..(140)
<223> "Xaa" at position 140 can be either Ile or Val.

<220>
<221> MISC_FEATURE
<222> (141)..(141)
<223> "Xaa" at position 141 can be either Leu or Met.

<220>
<221> MISC_FEATURE
<222> (142)..(142)
<223> "Xaa" at position 142 can be either Gln or Gly.

<220>
<221> MISC_FEATURE
<222> (143)..(143)
<223> "Xaa" at position 143 can be either Lys or His.

<220>
<221> MISC_FEATURE
<222> (145)..(145)
<223> "Xaa" at position 145 can be either Leu or Ile.

<220>
<221> MISC_FEATURE
<222> (146)..(146)
<223> "Xaa" at position 146 can be either Leu or Glu.

<220>
<221> MISC_FEATURE
<222> (147)..(147)
<223> "Xaa" at position 147 can be either Gly or Tyr.

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> "Xaa" at position 149 can be either Glu or Tyr.

<220>
<221> MISC_FEATURE
<222> (150)..(150)

<223> "Xaa" at position 150 can be either Pro or Asn.

<220>

<221> MISC_FEATURE

<222> (152)..(152)

<223> "Xaa" at position 152 can be either His or Phe.

<220>

<221> MISC_FEATURE

<222> (153)..(153)

<223> "Xaa" at position 153 can be either Asn or Glu.

<220>

<221> MISC_FEATURE

<222> (156)..(156)

<223> "Xaa" at position 156 can be either Tyr or Ile.

<220>

<221> MISC_FEATURE

<222> (158)..(158)

<223> "Xaa" at position 158 can be either Asn or Ala.

<220>

<221> MISC_FEATURE

<222> (165)..(165)

<223> "Xaa" at position 165 can be either Val or Ile.

<220>

<221> MISC_FEATURE

<222> (166)..(166)

<223> "Xaa" at position 166 can be either Lys or Leu.

<220>

<221> MISC_FEATURE

<222> (168)..(168)

<223> "Xaa" at position 168 can be either Gly or Asn.

<220>

<221> MISC_FEATURE

<222> (169)..(169)

<223> "Xaa" at position 169 can be either Glu or Phe.

<220>

<221> MISC_FEATURE

<222> (170)..(170)

<223> "Xaa" at position 170 can be either Lys or Val.

<220>
<221> MISC_FEATURE
<222> (172)..(172)
<223> "Xaa" at position 172 can be either Leu or Arg.

<220>
<221> MISC_FEATURE
<222> (173)..(173)
<223> "Xaa" at position 173 can be either Val or His.

<220>
<221> MISC_FEATURE
<222> (174)..(174)
<223> "Xaa" at position 174 can be either Asn or Tyr.

<220>
<221> MISC_FEATURE
<222> (175)..(175)
<223> "Xaa" at position 175 can be either Lys or Ile.

31
<220>
<221> MISC_FEATURE
<222> (176)..(176)
<223> "Xaa" at position 176 can be either Leu or Glu.

<220>
<221> MISC_FEATURE
<222> (178)..(179)
<223> "Xaa" at positions 178-179 can be either Ser or Gly.

<220>
<221> MISC_FEATURE
<222> (181)..(181)
<223> "Xaa" at position 181 can be either Tyr or Gln.

<220>
<221> MISC_FEATURE
<222> (182)..(182)
<223> "Xaa" at position 182 can be either Tyr or Glu.

<220>
<221> MISC_FEATURE
<222> (183)..(183)
<223> "Xaa" at position 183 can be either Ser or Ala.

<220>
<221> MISC_FEATURE
<222> (184)..(184)

<223> "Xaa" at position 184 can be either Cys or Asp.

<220>

<221> MISC_FEATURE

<222> (186)..(186)

<223> "Xaa" at position 186 can be either Met or Tyr.

<220>

<221> MISC_FEATURE

<222> (187)..(187)

<223> "Xaa" at position 187 can be either Lys or Gln.

<220>

<221> MISC_FEATURE

<222> (188)..(188)

<223> "Xaa" at position 188 can be either Thr or Gln.

<220>

<221> MISC_FEATURE

<222> (192)..(192)

<223> "Xaa" at position 192 can be either Ser or Ile.

<220>

<221> MISC_FEATURE

<222> (193)..(193)

<223> "Xaa" at position 193 can be either Lys or Gly.

<220>

<221> MISC_FEATURE

<222> (194)..(194)

<223> "Xaa" at position 194 can be either Asp or Gly.

<220>

<221> MISC_FEATURE

<222> (196)..(196)

<223> "Xaa" at position 196 can be either Val or Pro.

<220>

<221> MISC_FEATURE

<222> (197)..(197)

<223> "Xaa" at position 197 can be either Val or Lys.

<220>

<221> MISC_FEATURE

<222> (198)..(198)

<223> "Xaa" at position 198 can be either Glu or Leu.

<220>
<221> MISC_FEATURE
<222> (199)..(199)
<223> "Xaa" at position 199 can be either Phe or Leu.

<220>
<221> MISC_FEATURE
<222> (202)..(202)
<223> "Xaa" at position 202 can be either Tyr or Asn.

<220>
<221> MISC_FEATURE
<222> (204)..(204)
<223> "Xaa" at position 204 can be either Phe or Tyr.

<220>
<221> MISC_FEATURE
<222> (205)..(205)
<223> "Xaa" at position 205 can be either Ile or Leu.

CB1
<220>
<221> MISC_FEATURE
<222> (209)..(209)
<223> "Xaa" at position 209 can be either Thr or Leu.

<220>
<221> MISC_FEATURE
<222> (210)..(210)
<223> "Xaa" at position 210 can be either Glu or Gln.

<220>
<221> MISC_FEATURE
<222> (211)..(211)
<223> "Xaa" at position 211 can be either Ser or Lys.

<220>
<221> MISC_FEATURE
<222> (212)..(212)
<223> "Xaa" at position 212 can be either Thr or Ala.

<220>
<221> MISC_FEATURE
<222> (213)..(213)
<223> "Xaa" at position 213 can be either Tyr or Leu.

<220>
<221> MISC_FEATURE
<222> (214)..(214)

<223> "Xaa" at position 214 can be either Val or Ser.

<220>

<221> MISC_FEATURE

<222> (215)..(215)

<223> "Xaa" at position 215 can be either Glu or Lys.

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> "Xaa" at position 217 can be either Gly or Pro.

<220>

<221> MISC_FEATURE

<222> (219)..(219)

<223> "Xaa" at position 219 can be either Phe or Glu.

<220>

<221> MISC_FEATURE

<222> (220)..(220)

<223> "Xaa" at position 220 can be either Val or Lys.

<220>

<221> MISC_FEATURE

<222> (221)..(221)

<223> "Xaa" at position 221 can be either Glu or Arg.

<220>

<221> MISC_FEATURE

<222> (222)..(222)

<223> "Xaa" at position 222 can be either Gln or Asp.

<220>

<221> MISC_FEATURE

<222> (224)..(224)

<223> "Xaa" at position 222 can be either Glu or Met.

<220>

<221> MISC_FEATURE

<222> (225)..(225)

<223> "Xaa" at position 225 can be either Thr or Val.

<220>

<221> MISC_FEATURE

<222> (226)..(226)

<223> "Xaa" at position 226 can be either Ala or Leu.

<220>
<221> MISC_FEATURE
<222> (227)..(227)
<223> "Xaa" at position 227 can be either Ile or Leu.

<220>
<221> MISC_FEATURE
<222> (228)..(228)
<223> "Xaa" at position 228 can be either Ala or Glu.

<220>
<221> MISC_FEATURE
<222> (229)..(229)
<223> "Xaa" at position 229 can be either Gln or Phe.

<220>
<221> MISC_FEATURE
<222> (233)..(233)
<223> "Xaa" at position 233 can be either Ile or Ala.

B1
<220>
<221> MISC_FEATURE
<222> (235)..(235)
<223> "Xaa" at position 235 can be either Ile or Lys.

<220>
<221> MISC_FEATURE
<222> (236)..(236)
<223> "Xaa" at position 236 can be either Pro or Tyr.

<220>
<221> MISC_FEATURE
<222> (239)..(239)
<223> "Xaa" at position 239 can be either Ser or Met.

<220>
<221> MISC_FEATURE
<222> (240)..(240)
<223> "Xaa" at position 240 can be either Leu or Asp.

<220>
<221> MISC_FEATURE
<222> (241)..(241)
<223> "Xaa" at position 241 can be either Glu or His.

<220>
<221> MISC_FEATURE
<222> (242)..(242)

<223> "Xaa" at position 242 can be either Glu or Leu.

<220>

<221> MISC_FEATURE

<222> (243)..(243)

<223> "Xaa" at position 243 can be either Trp or Tyr.

<220>

<221> MISC_FEATURE

<222> (244)..(244)

<223> "Xaa" at position 244 can be either Val or Lys.

<400> 8

Met Ser Lys Gly Glu Xaa Xaa Xaa Thr Gly Xaa Val Xaa Ile Xaa Ser
1 5 10 15

Xaa Lys Val Glu Leu Xaa Gly Xaa Val Asn Xaa His Xaa Phe Ser Xaa
20 25 30

Xaa Gly Glu Gly Xaa Gly Xaa Ala Xaa Xaa Gly Xaa Xaa Xaa Leu Xaa
35 40 45

Xaa Xaa Xaa Thr Xaa Gly Xaa Xaa Leu Pro Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Thr Xaa Phe Gln Tyr Gly Xaa Xaa Xaa Phe Xaa Xaa Tyr Pro Asp
65 70 75 80

Xaa Xaa Lys Gln His Asp Xaa Phe Lys Xaa Xaa Xaa Pro Xaa Gly Xaa
85 90 95

Val Xaa Glu Arg Thr Xaa Xaa Phe Xaa Asp Xaa Gly Asn Xaa Lys Xaa
100 105 110

Arg Xaa Xaa Xaa Lys Xaa Glu Gly Asp Xaa Xaa Val Xaa Arg Xaa Glu
115 120 125

Xaa Lys Gly Ile Asp Phe Xaa Glu Asp Gly Xaa Xaa Xaa Xaa Lys
130 135 140

Xaa Xaa Xaa Asn Xaa Xaa Ser Xaa Xaa Val Tyr Xaa Met Xaa Asp Lys
145 150 155 160

Gln Lys Asn Gly Xaa Xaa Val Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
 165 170 175

Asp Xaa Xaa Val Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Asn Thr Pro Xaa
 180 185 190

Xaa Xaa Gly Xaa Xaa Xaa Xaa Pro Asp Xaa His Xaa Xaa Ser His Arg
 195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Asn Xaa Xaa Xaa Xaa His Xaa
 210 215 220

Xaa Xaa Xaa Xaa Xaa Val Thr Ala Xaa Gly Xaa Xaa Leu Gly Xaa Xaa
 225 230 235 240

Xaa Xaa Xaa Xaa

<210> 9
 <211> 61
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> coiled coil structure

<400> 9

Met Gly Cys Ala Ala Leu Glu Ser Glu Val Ser Ala Leu Glu Ser Glu
 1 5 10 15

Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Gly Arg Gly Asp Met
 20 25 30

Pro Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys Ser Lys Leu
 35 40 45

Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Pro Pro
 50 55 60

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> loop structure

<400> 10

Gly Arg Gly Asp Met Pro
1 5

<210> 11

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> minibody presentation structure

<400> 11

Met Gly Arg Asn Ser Gln Ala Thr Ser Gly Phe Thr Phe Ser His Phe
1 5 10 15

Tyr Met Glu Trp Val Arg Gly Gly Glu Tyr Ile Ala Ala Ser Arg His
20 25 30

Lys His Asn Lys Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg
35 40 45

Tyr Ile Val Ser Arg Asp Thr Ser Gln Ser Ile Leu Tyr Leu Gln Lys
50 55 60

Lys Lys Gly Pro Pro
65

<210> 12

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Preferred C2H2 zinc finger sequence

<220>

<221> MISC_FEATURE

<222> (7)..(26)

<223> "Xaa" at positions 7 through 26 is a random peptide any 3 to 20 amino acids

<400> 12

Phe Gln Cys Glu Glu Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Ile Arg Ser His Thr
 20 25 30

Gly

<210> 13
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Preferred CCHC box based on nucleocapsid protein P2

<220>
 <221> MISC_FEATURE
 <222> (7)..(26)
 <223> "Xaa" at positions 7 through 26 can be any 4 to 20 random amino acids.

<400> 13

Val Lys Cys Phe Asn Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Thr Ala Arg Asn Cys
 20 25 30

Arg

<210> 14
 <211> 34
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Preferred CCHC box based on the nmr structural ensemble 1ZFP.

<220>
 <221> MISC_FEATURE
 <222> (10)..(29)
 <223> "Xaa" at positions 10-29 can be any 4 to 20 random amino acids.

<400> 14

Met Asn Pro Asn Cys Ala Arg Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Lys Ala
 20 25 30

Cys Phe

<210> 15
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> dimerization sequence
 <400> 15

Glu Phe Leu Ile Val Lys Ser
 1 5

<210> 16
 <211> 9
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> dimerization sequence
 <400> 16

Glu Glu Phe Leu Ile Val Lys Lys Ser
 1 5

<210> 17
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> dimerization sequence
 <400> 17

Phe Glu Ser Ile Lys Leu Val
 1 5

<210> 18
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> dimerization sequence

<400> 18

Val Ser Ile Lys Phe Glu Leu
1 5

<210> 19

<211> 7

<212> PRT

<213> Simian virus 40

<400> 19

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 20

<211> 6

<212> PRT

<213> Homo sapiens

<400> 20

Ala Arg Arg Arg Arg Pro
1 5

<210> 21

<211> 10

<212> PRT

<213> Mus musculus

<400> 21

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 22

<211> 9

<212> PRT

<213> Mus musculus

<400> 22

Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 23

<211> 20

<212> PRT

<213> Xenopus laevis

<400> 23

Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1 5 10 15

Lys Lys Leu Asp
20

<210> 24

<211> 31

<212> PRT

<213> Mus musculus

<400> 24

Met Ala Ser Pro Leu Thr Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu
1 5 10 15

Gly Glu Ser Ile Leu Gly Ser Gly Glu Ala Lys Pro Gln Ala Pro
20 25 30

B1 <210> 25

<211> 21

<212> PRT

<213> Homo sapiens

<400> 25

Met Ser Ser Phe Gly Tyr Arg Thr Leu Thr Val Ala Leu Phe Thr Leu
1 5 10 15

Ile Cys Cys Pro Gly
20

<210> 26

<211> 51

<212> PRT

<213> Mus musculus

<400> 26

Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr
1 5 10 15

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
20 25 30

Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr
35 40 45

His Ser Arg
50

<210> 27
<211> 33
<212> PRT
<213> Homo sapiens

<400> 27

Met Val Ile Ile Val Thr Val Val Ser Val Leu Leu Ser Leu Phe Val
1 5 10 15

Thr Ser Val Leu Leu Cys Phe Ile Phe Gly Gln His Leu Arg Gln Gln
20 25 30

Arg

31
<210> 28
<211> 37
<212> PRT
<213> Rattus sp.

<400> 28

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
35

<210> 29
<211> 14
<212> PRT
<213> Homo sapiens

<400> 29

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 30
<211> 26

<212> PRT
<213> Homo sapiens

<400> 30

Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg Leu
20 25

<210> 31
<211> 20
<212> PRT
<213> Rattus norvegicus

<400> 31

Lys Gln Phe Arg Asn Cys Met Leu Thr Ser Leu Cys Cys Gly Lys Asn
1 5 10 15

Pro Leu Gly Asp
20

<210> 32
<211> 19
<212> PRT
<213> Homo sapiens

<400> 32

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> lysomal degradation sequence

<400> 33

Lys Phe Glu Arg Gln
1 5

<210> 34
<211> 36
<212> PRT
<213> Cricetulus griseus

<400> 34

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
20 25 30

Tyr Gln Thr Ile
35

<210> 35
<211> 35
<212> PRT
<213> Homo sapiens

<400> 35

Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 36
<211> 27
<212> PRT
<213> yeast

<400> 36

Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 37
<211> 25
<212> PRT
<213> yeast

<400> 37

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

<210> 38

<211> 64

<212> PRT

<213> yeast

<400> 38

Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
20 25 30

Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
35 40 45

Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
50 55 60

<210> 39

<211> 41

<212> PRT

<213> yeast

<400> 39

Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
1 5 10 15

Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
20 25 30

Gln Gln Gln Gln Arg Gly Lys Lys
35 40

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> endoplasmic reticulum sequence

<400> 40

Lys Asp Glu Leu

1

<210> 41

<211> 15

<212> PRT

<213> adenovirus

<400> 41

Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
1 5 10 15

<210> 42

<211> 19

<212> PRT

<213> Mus sp.

<400> 42

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 43

<211> 15

<212> PRT

<213> Homo sapiens

<400> 43

Leu Thr Glu Pro Thr Gln Pro Thr Arg Asn Gln Cys Cys Ser Asn
1 5 10 15

<210> 44

<211> 9

<212> PRT

<213> Homo sapiens

<400> 44

Arg Thr Ala Leu Gly Asp Ile Gly Asn
1 5

<210> 45
<211> 20
<212> PRT
<213> Homo sapiens

<400> 45

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 46
<211> 29
<212> PRT
<213> Homo sapiens

<400> 46

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 47
<211> 27
<212> PRT
<213> Homo sapiens

<400> 47

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 48
<211> 18
<212> PRT
<213> Influenza virus

<400> 48

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 49
<211> 24
<212> PRT
<213> Homo sapiens

<400> 49

Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
20

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> purification sequence

<400> 50

His His His His His His
1 5

<210> 51
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> stability sequence

<220>
<221> MISC_FEATURE
<222> (3)..(6)
<223> "Xaa" at postions 3 through 6 is a peptide having at least 4 residues of any amino acid.

<400> 51

Met Gly Xaa Xaa Xaa Xaa Gly Gly Pro Pro
1 5 10

<210> 52
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 52

Gly Ser Gly Gly Ser
1 5

<210> 53

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 53

Gly Gly Gly Ser
1

<210> 54

<211> 9

<212> PRT

<213> Xenopus laevis

<400> 54

Arg Thr Val Leu Gly Val Ile Gly Asp
1 5

<210> 55

<211> 9

<212> PRT

<213> Homo sapiens

<400> 55

Arg Thr Ala Leu Gly Ile Asp Gly Asn
1 5

<210> 56

<211> 27

<212> PRT

<213> Rattus sp.

<400> 56

Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
1 5 10 15

Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
20 25

<210> 57
<211> 28
<212> PRT
<213> Mus sp.

<400> 57

Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
1 5 10 15

Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
20 25

<210> 58
<211> 27
<212> PRT
<213> Mus sp.

<400> 58

Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg
1 5 10 15

Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
20 25

<210> 59
<211> 27
<212> PRT
<213> Mus sp.

<400> 59

Asp Arg Phe Leu Gln Ala Gln Leu Val Cys Arg Lys Lys Leu Gln Val
1 5 10 15

Val Gly Ile Thr Ala Leu Leu Leu Ala Ser Lys
20 25

<210> 60
<211> 18
<212> PRT
<213> Mus sp.

<400> 60

Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met
 1 5 10 15

Leu Leu

<210> 61
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 61

Glu Glu Ala Ala Lys Ala
 1 5

<210> 62
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 62
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<210> 63
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Pro Leu Gly Ser Glu Phe
1 5

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Gly Pro Leu Gly Ser
1 5

B1
Cm
